



## results of BLAST

## BLASTN 2.2.6 [Apr-09-2003]

RID: 1064960959-20664-530139.BLASTQ3

## Query=

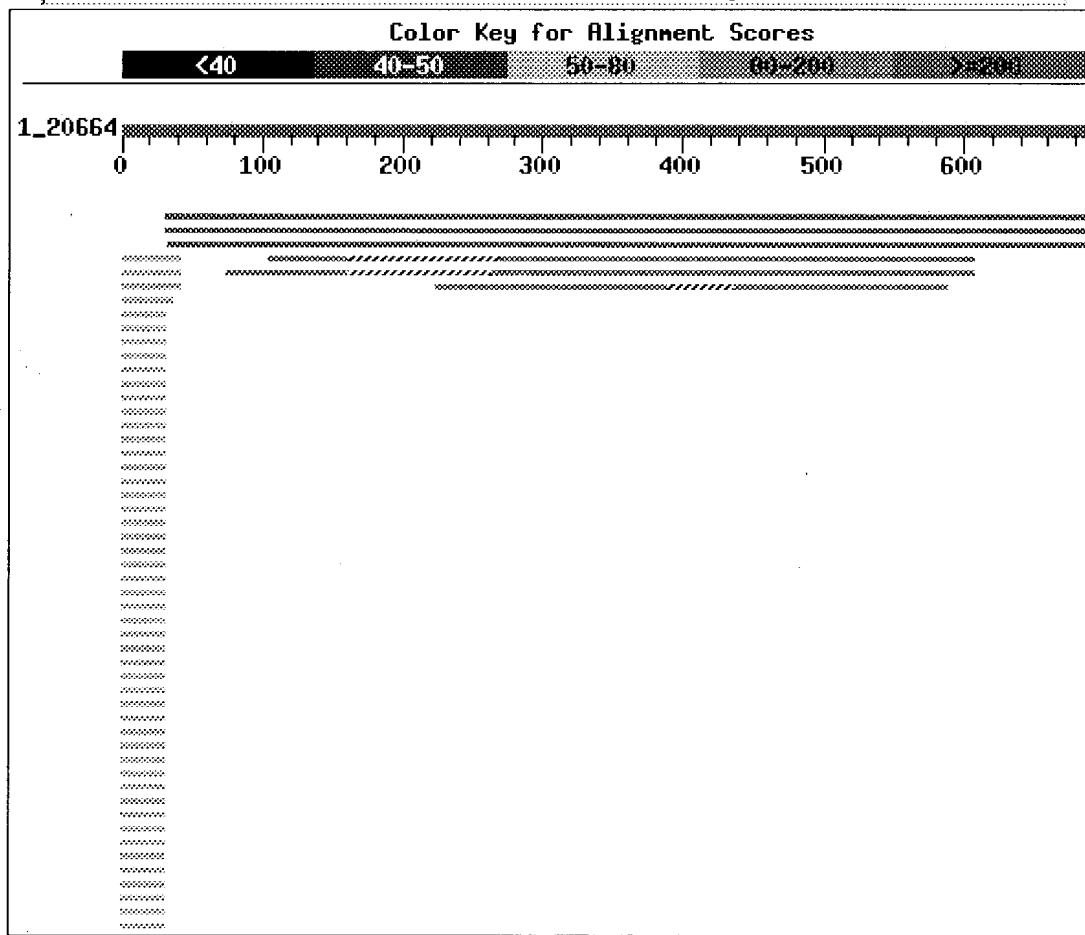
(689 letters)

**Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)

1,931,681 sequences; 9,156,315,655 total letters

Taxonomy reportsDistribution of 106 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E  
(bits) Value

gi 505280 emb X59040.1 CBDPEXC3	Clostridium botulinum D pha...	1261	0.0
gi 296786 emb X59039.1 CBCPEXC3	Clostridium botulinum C pha...	1261	0.0
gi 149071 emb X51464.1 CBDPE3	Clostridium botulinum D Phage ...	1257	0.0
gi 144736 gb M74038.1 CLOC3ADP	C.botulinum C3 ADP-ribosyltr...	184	1e-43
gi 404820 dbj D17555.1 CLOADPRC3	Clostridium botulinum type...	172	5e-40
gi 1212874 emb X87215.1 CLC3GENE	C.limosum C3 gene	100	6e-18
gi 33149672 gb AY330212.1	Cloning vector pT3, complete seq...	68	2e-08
gi 595779 gb U13871.1 XXU13871	pT7T3D cloning vector, compl...	68	2e-08
gi 595774 gb U13869.1 XXU13869	pT7T318U cloning vector, com...	68	2e-08
gi 1149706 emb X86491.1 CPSFOOA	C.perfringens spoOA gene	66	9e-08
gi 31335236 gb AY292466.1	BAC cloning vector pBACVM4, comp...	64	3e-07
gi 30424554 gb AY182782.1	Shuttle vector pSK5640, complete...	64	3e-07
gi 30424549 gb AY182781.1	Shuttle vector pSK5632, complete...	64	3e-07
gi 29838547 gb AY265466.1	Shuttle vector pAM2770, complete...	64	3e-07
gi 29825787 gb AY263154.1	Cloning vector pAM2600, complete...	64	3e-07
gi 29415162 gb AY150268.1	CRIM plasmid pSK67, complete seq...	64	3e-07
gi 29373934 gb AY219701.1	Cloning vector pAZ1, complete se...	64	3e-07
gi 22595311 gb AF405697.1	Reporter vector pALH122, complet...	64	3e-07
gi 28207668 gb AY1827276.1	Shuttle vector pBSV2, complete s...	64	3e-07
gi 21952452 gb AF524829.1	P-element cloning system vector ...	64	3e-07
gi 21952450 gb AF524828.1	P-element cloning system vector ...	64	3e-07
gi 21780275 gb AF521666.1	Cloning vector pLOI2065 complete...	64	3e-07
gi 25141017 gb AC116033.2	Zea mays genomic clone ZM15C05 ...	64	3e-07
gi 22074797 gb AY112734.1	Broad host range vector pMLS7, c...	64	3e-07
gi 22074788 gb AY112733.1	Broad host range vector pMLBAD, ...	64	3e-07
gi 5824688 emb AL110477.1 CEY113G7B	Caenorhabditis elegans ...	64	3e-07
gi 34556140 emb BX005348.8	Zebrafish DNA sequence from clo...	64	3e-07
gi 33457134 emb AJ560658.1 SSC560658	Sus scrofa partial mRN...	64	3e-07
gi 4567137 gb AF134471.1	Homo sapiens chromosome 10 clone ...	64	3e-07
gi 21617574 gb AF519766.1	Cloning vector pMAK705, complete...	64	3e-07
gi 21328627 gb AE008921.1	Uncultured proteobacterium clone...	64	3e-07
gi 11559661 gb AF294973.1	Cloning vector pc1300intC, compl...	64	3e-07
gi 11559659 gb AF294977.1	Cloning vector pc1300intB, compl...	64	3e-07
gi 11559657 gb AF294976.1	Cloning vector pc1300intA, compl...	64	3e-07
gi 20141090 gb L09137.2 SYNPUC19CV	Cloning vector pUC19c, c...	64	3e-07
gi 20455693 gb AC110750.4	Homo sapiens chromosome 17, clon...	64	3e-07
gi 5419758 emb AJ246004.1 HSA246004	Homo sapiens RET gene, ...	64	3e-07
gi 18766962 gb AF480833.1	Cloning vector pNOT218 beta-lact...	64	3e-07
gi 18654300 gb L47837.1 SYNKIL199F	Cloning vector pKIL199 c...	64	3e-07
gi 18654298 gb L47836.1 SYNKIL198P	Cloning vector pKIL198 c...	64	3e-07
gi 14794622 gb AF327719.1 AF327719	Cloning vector pCM130, c...	64	3e-07
gi 14794608 gb AF327717.1 AF327717	Cloning vector pCM160, c...	64	3e-07
gi 14794600 gb AF327716.1 AF327716	Cloning vector pCM80, co...	64	3e-07
gi 14794593 gb AF327715.1 AF327715	Cloning vector pCM66, co...	64	3e-07
gi 14794585 gb AF327714.1 AF327714	Cloning vector pCM62, co...	64	3e-07
gi 14794547 gb AF327711.1 AF327711	Cloning vector pDN19, co...	64	3e-07
gi 18041969 gb AF337031.1 AF337031	Aphidius ervi clone 110 ...	64	3e-07
gi 18041957 gb AF337016.1 AF337016	Aphidius ervi clone 34 m...	64	3e-07
gi 18041950 gb AF337003.1 AF337003	Aphidius ervi clone 13R ...	64	3e-07
gi 18041946 gb AF336997.1 AF336997	Aphidius ervi clone 107 ...	64	3e-07
gi 18041941 gb AF336992.1 AF336992	Aphidius ervi clone 47 m...	64	3e-07
gi 18041939 gb AF336990.1 AF336990	Aphidius ervi clone 4 mi...	64	3e-07
gi 13161000 gb AF325903.1 AF325903	Cloning vector pFH2191, ...	64	3e-07
gi 13540351 gb AF354046.1 AF354046	Binary vector pCAMBIA-13...	64	3e-07
gi 13540346 gb AF354045.1 AF354045	Binary vector pCAMBIA-13...	64	3e-07
gi 13345295 gb AF323603.1 AF323603	Cloning vector pPOP, com...	64	3e-07
gi 8308058 gb AF261959.1 AF261959	Anourosorex squamipes clo...	64	3e-07
gi 9294791 gb AF178451.1 AF178451	Integration vector pCD11P...	64	3e-07
gi 8927566 gb AF276982.1 AF276982	Integrative vector pNLE1,...	64	3e-07

gi 8650401 gb AF216802.1 AF216802	Shuttle vector pDL278, co...	64	3e-07
gi 8272485 gb AF219942.1 AF219942	Shuttle vector pPha-T1 co...	64	3e-07
gi 7715975 gb AF203972.1 AF203972	Shuttle vector pBA comple...	64	3e-07
gi 7705080 gb AC068564.1 AC068564	Filobasidiella neoformans...	64	3e-07
gi 5689998 emb AJ131112.1 SSC131112	Sus scrofa MHC class I ...	64	3e-07
gi 28300623 emb AL953891.101	Zebrafish DNA sequence from cl...	64	3e-07
gi 7638149 gb AF234316.1 AF234316	Binary vector pCAMBIA-230...	64	3e-07
gi 7638145 gb AF234315.1 AF234315	Binary vector pCAMBIA-230...	64	3e-07
gi 7638140 gb AF234314.1 AF234314	Binary vector pCAMBIA-220...	64	3e-07
gi 7638136 gb AF234313.1 AF234313	Binary vector pCAMBIA-220...	64	3e-07
gi 7638083 gb AF234300.1 AF234300	Binary vector pCAMBIA-130...	64	3e-07
gi 7638078 gb AF234299.1 AF234299	Binary vector pCAMBIA-130...	64	3e-07
gi 7638073 gb AF234298.1 AF234298	Binary vector pCAMBIA-130...	64	3e-07
gi 7638068 gb AF234297.1 AF234297	Binary vector pCAMBIA-130...	64	3e-07
gi 7638064 gb AF234296.1 AF234296	Binary vector pCAMBIA-130...	64	3e-07
gi 7638049 gb AF234293.1 AF234293	Binary vector pCAMBIA-120...	64	3e-07
gi 7638045 gb AF234292.1 AF234292	Binary vector pCAMBIA-120...	64	3e-07
gi 7415878 dbj AB038146.1	Cloning vector pGFPTA DNA, compl...	64	3e-07
gi 27531019 dbj AB082961.1	Cloning vector pMG171 DNA, comp...	64	3e-07
gi 27531016 dbj AB082960.1	Cloning vector pMG170 DNA, comp...	64	3e-07
gi 15553040 dbj AB055652.1	Thermosensitive suicide vector ...	64	3e-07
gi 15553035 dbj AB055651.1	Thermosensitive suicide vector ...	64	3e-07
gi 15553030 dbj AB055650.1	Thermosensitive suicide vector ...	64	3e-07
gi 8250423 emb AJ271043.1 MBA271043	Marine bacterium S5 par...	64	3e-07
gi 4884786 gb AF128862.1 AF128862	Cloning vector pHIND2.2, ...	64	3e-07
gi 4731624 gb AF134573.1 AF134573	Cloning vector p34S-Sm3, ...	64	3e-07
gi 4731621 gb AF134572.1 AF134572	Cloning vector p34S-Sm2, ...	64	3e-07
gi 3907623 gb AF102233.1 AF102233	Transposon delivery vecto...	64	3e-07
gi 3136321 gb AF064067.1 AF064067	Expression vector pYZ81N,...	64	3e-07
gi 3136317 gb AF064066.1 AF064066	Expression vector pYZ41N,...	64	3e-07
gi 29164976 gb AY219695.1	Shuttle vector pBHT18mob2, compl...	64	3e-07
gi 29164973 gb AY219694.1	Shuttle vector pBHK18mob2, compl...	64	3e-07
gi 29164970 gb AY219693.1	Shuttle vector pBHC18mob2, compl...	64	3e-07
gi 29164967 gb AY219692.1	Shuttle vector pBHT18, complete ...	64	3e-07
gi 29164964 gb AY219691.1	Shuttle vector pBHK18, complete ...	64	3e-07
gi 29164961 gb AY219690.1	Shuttle vector pBHC18, complete ...	64	3e-07
gi 29164958 gb AY219689.1	Expression vector pXT99A, comple...	64	3e-07
gi 29164955 gb AY219688.1	Expression vector pXS99A, comple...	64	3e-07
gi 29164951 gb AY219687.1	Expression vector pXK99CAT, comp...	64	3e-07
gi 4827116 dbj AP000150.1	Homo sapiens genomic DNA, chromo...	64	3e-07
gi 6468567 emb AJ131034.1 HSA131034	Homo sapiens otase gene...	58	2e-05

## Alignments

### Get selected sequences

Select all

Deselect all

>gi|5052801emb|X59040.1|CBDPEXC3 Clostridium botulinum D phage gene for exoenzyme

Score = 1261 bits (636), Expect = 0.0  
Identities = 654/659 (99%), Gaps = 1/659 (0%)  
Strand = Plus / Plus

Query: 32 atgcttattccattaatcaaa-ggcttattcaaatacttaccaggagttactaatattg 90

Sbjct: 823 atgcttattccattaatcaaaaggcttattcaaatacttaccaggagttactaatattg 882

Query: 91 atcaagcaaaagctgggtaatgctcagtataaaaagtatggactaagcaaatcagaaa 150  
Sbjct: 883 atcaagcaaaagctgggtaatgctcagtataaaaagtatggactaagcaaatcagaaa 942

Query: 151 aagaagctatagtatcatatactaaaagcgctagtgaaataatggaaagctaagacaaa 210  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 943 aagaagctatagtatcatatactaaaqcgcgtatgaaaataatggaaagctaagacaaa 1002

Query: 211 ataaggagttatcaatggattccttcaattataaaaacaagttgaacttttagata 270  
          |||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 1003 ataaggagttatcaatggattccttcaattataaaaacaagttgaacttttagata 1062

Query: 271 aatctttataaaaaatgaagaccctgaaaaatattatgttatttagaggcgacgaccctg 330  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 1063 aatctttataaaaaatgaagaccctgaaaaatattatgttatttagaggcgacgaccctg 1122

Query: 511 aagttagcaaaaggctcaaaggcaggatattgaccctatttagtgctttcagggacaac 570  
|||||||  
Subject: 1202 aagttagcaaaaggctcaaaggcaggatattgaccctatttagtgctttcagggacaac 1262  
|||||||

[>]gi|296786|emb|X59039.1|CBCPEXC3 Clostridium botulinum C phage gene for exoenzyme  
Length = 1977

Score = 1261 bits (636), Expect = 0.0  
Identities = 654/659 (99%), Gaps = 1/659 (0%)  
Strand = Plus / Plus

Query: 32 atgcttattccattaatcaaa-ggcttattcaaatacttaccaggagttactaatattg 90  
||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 821 atgcttattccattaatcaaaaggcttattcaaatacttaccaggagttactaatattg 880

Query: 91 atcaagcaaaagcttgggtaatgctcagtataaaaagtatggactaagcaatcagaaa 150  
||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||  
Sbjct: 881 atcaagcaaaagcttgggtaatgctcagtataaaaagtatggactaagcaatcagaaa 940

Query: 151 aagaagctatagtatcatatactaaaagcgctagtgaaataatggaaagctaagacaaa 210  
||||||||||||||||||| |||||||||||||||||||||||||||||||||||  
Sbjct: 941 aagaagctatagtatcatatactaaaagcgctagtgaaataatggaaagctaagacaaa 1000

Query: 211 ataaggagttatcaatggattcctcaaattataaaaacaagttgaacttttagata 270  
||||||||||||||||||| |||||||||||||||||||||||||||||||  
Sbjct: 1001 ataaggagttatcaatggattcctcaaattataaaaacaagttgaacttttagata 1060

Query: 271 aatctttaataaaatgaagaccctgaaaatattatgttatttagaggcgacgaccctg 330  
||||||||||||||||||| |||||||||||||||||||||||||||  
Sbjct: 1061 aatctttaataaaatgaagaccctgaaaatattatgttatttagaggcgacgaccctg 1120

Query: 331 ctatatttaggaacagaattcaaaacactcttcttaattcaaattgtacaattaataaaa 390  
||||||||||||||||||| |||||||||||||||||||||||  
Sbjct: 1121 ctatatttaggaacagaattcaaaacactcttcttaattcaaattgtacaattaataaaa 1180

Query: 391 cggctttgaaaaggctaaagctaagtttaataaagatagacttgaatatggatata 450  
||||||||||||||||||| |||||||||||||||||||  
Sbjct: 1181 cggctttgaaaaggctaaagctaagtttaataaagatagacttgaatatggatata 1240

Query: 451 tttagtacttcattaatgaatgttctcaatttcaggaagaccaattttacanaattt 510  
||||||||||||||||||| |||||||||||||||||||  
Sbjct: 1241 tttagtacttcattaatgaatgttctcaatttcaggaagaccaattttacaaaattt 1300

Query: 511 aagtagcaaaaggctaaaggcaggatattgaccctattgtgtttcaggacaac 570  
||||||||||||||||||| |||||||  
Sbjct: 1301 aagtagcaaaaggctaaaggcaggatattgaccctattgtgtttcaggacaac 1360

Query: 571 ttgaaatgttgccttagacatagttacttatcatatagacgatgatggattgtctctg 630  
||||||||||||||||||| |||||||||||||||  
Sbjct: 1361 ttgaaatgttgccttagacatagttacttatcatatagacgatgatggattgtctctg 1420

Query: 631 atgttaaacaataataattacagcaacaatgtggcacagctatcaatcctaaataa 689  
|||||||||||||||||||  
Sbjct: 1421 atgttaaacaataataattacagcaacaatgtggcacagctatcaatcctaaataa 1479

gi|14907|emb|X51464.1|CBDPE3 Clostridium botulinum D Phage C3 gene for exoenzyme  
Length = 780

Score = 1257 bits (634), Expect = 0.0  
Identities = 652/657 (99%), Gaps = 1/657 (0%)  
Strand = Plus / Plus

Query: 34 gcttattccattaatcaaa-ggcttattcaaatacttaccaggagttactaatattgat 92  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 1 gcttattccattaatcaaaaggcttattcaaatacttaccaggagttactaatattgat 60

Query: 93 caagcaaaagcttgggtaatgctcagtataaaaagtatggactaagcaaatcagaaaaa 152  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 61 caagcaaaagcttgggtaatgctcagtataaaaagtatggactaagcaaatcagaaaaa 120

Query: 153 gaagctatagtatcatatactaaaagcgctagtgaaataatggaaagctaaagacaaaat 212  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 121 gaagctatagtatcatatactaaaagcgctagtgaaataatggaaagctaaagacaaaat 180

Query: 213 aaggagtttatcaatggatttccttcaaatttaataaaaacaagttgaacttttagataaa 272  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 181 aaggagtttatcaatggatttccttcaaatttaataaaaacaagttgaacttttagataaa 240

Query: 273 tcttttaataaaatgaagaccctgaaaatattatgttatttagaggcgacgaccctgct 332  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 241 tcttttaataaaatgaagaccctgaaaatattatgttatttagaggcgacgaccctgct 300

Query: 333 tatttaggaacagaatttcaaaacactcttcttaattcaaatggtacaattaataaaaacg 392  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 301 tatttaggaacagaatttcaaaacactcttcttaattcaaatggtacaattaataaaaacg 360

Query: 393 gctttgaaaaggctaaagctaagttttaaataaagatagacttgaatatggatattt 452  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 361 gctttgaaaaggctaaagctaagttttaaataaagatagacttgaatatggatattt 420

Query: 453 agtacttcattaatgaatgttctcaatttgcaggaagaccaattttacanaatttaaa 512  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 421 agtacttcattaatgaatgttctcaatttgcaggaagaccaattttacaaaatttaaa 480

Query: 513 gtagcaaaaggctaaaggcaggatattgaccctatttagtgccttcaggacaactt 572  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 481 gtagcaaaaggctaaaggcaggatattgaccctatttagtgccttcaggacaactt 540

Query: 573 gaaatgttgcttcctagacatagttacttatcatatagacgatattgagattgtttctgat 632  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 541 gaaatgttgcttcctagacatagttacttatcatatagacgatattgagattgtttctgat 600

Query: 633 ggtaaacaataataattacagcaacaatgatggcacagctatcaatcctaataa 689  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 601 ggtaaacaataataattacagcaacaatgatggcacagctatcaatcctaataa 657

gi|144736|gb|M74038.1|CLOC3ADP C.botulinum C3 ADP-ribosyltransferase gene, comp  
Length = 2067

Score = 184 bits (93), Expect = 1e-43  
Identities = 277/338 (81%), Gaps = 3/338 (0%)  
Strand = Plus / Plus

Query: 271 aatctttataataaaatgaagaccctgaaaatattatgttatttagaggcgacgaccctg 330  
Sbjct: 772 aatcttttagtaagatgaagatgcctcaaaatattattcttttagaggtatgaccctg 831

Query: 331 cttatTTtaggaacagaattcaaaacactcttcttaattcaaTgtacaattaataaa 390  
Sbjct: 832 cttatTTtaggtccagaattcaagataaaattctaataaagatggaacaattaataaa 891

Query: 391 cggctttgaaaaggctaaagctaaagtTTtaataaagatagaCTGAATATGGATATA 450  
Sbjct: 892 ctgttttgaacaagttaaagcgaattttaaaaaggatagaacagaatatggatata 951

Query: 451 tttagtacttcattaatgaatgtttctcaattgcaggaagaccaattttacanaattta 510  
Sbjct: 952 tttagtacttcattaatgagtg---cgcaatttggaggaagaccaattgttactaaattta 1008

Query: 511 aagtagcaaaaggctcaaaggcaggatattgaccctattagtgcTTTcagggacaac 570  
Sbjct: 1009 aagtaactaatggatcaaaaggagggtatatagaccctattagctattcccaggacaac 1068

Query: 571 ttgaaatgtgcttcctagacatagttacttatcatata 608  
Sbjct: 1069 ttgaagtgtgcttcctagaaataatagttattatata 1106

Score = 58.0 bits (29), Expect = 2e-05  
Identities = 50/57 (87%)  
Strand = Plus / Plus

Query: 105 tgggtaatgctcagtataaaaagtatggactaagcaaattcagaaaaagaagctata 161  
Sbjct: 606 tgggaaatgctcaatataaaaatatggcctaagcaaaccctgaacaagaagctata 662

gi|404820|dbj|D17555.1|CLOADPRC3 Clostridium botulinum type D gene for ADP-ribo  
complete cds  
Length = 1712

Score = 172 bits (87), Expect = 5e-40  
Identities = 280/344 (81%), Gaps = 3/344 (0%)  
Strand = Plus / Plus

Query: 265 tagataaatcttttaataaaaatgaagacccctgaaaatattatgttatttagaggcgacg 324  
||||| |||||||| | ||| ||||||| ||| ||||||||| | ||||||||| ||| |  
Sbjct: 764 tagatcaatcttttagtaagatgaagatgcctcaaaatattattcttttagaggtgatg 823

Query: 325 accctgcttatttagaacagaattcaaaacacttttcaattcaaaatggtaacaatta 384  
||||||| ||||||| ||||| ||||| ||| ||| ||||| ||| ||| ||||| ||| ||||| |||||  
Sbjct: 824 accctgcttatttagtccagaattcaagataaaattttcaataaaatggatqqaacaatta 883

Query: 445 gatatattatgtacttcattaatgaatgttctcaattgcagggaaagaccaatttacan 504  
|||||||||||||||||||||| || | ||||||| ||||||||| ||||| |||||  
Sbjct: 944 gatatattatgtacttcattaatgaatgtg--cgcaattggggaaagaccaattgttacta 1000

Query: 505 aatttaaagttagcaaaaggctcaaaggcaggatattgaccctatttagtgctttcagg 564  
||||||| |||| | || || |||| | || || || || || || || || || || | |  
Sbjct: 1001 aatttaaagttaactaatggatcaaaaggagggtatatagaccctatttagtattttccagg 1060

Query: 565 gacaacttgaatgttgc~~tt~~c~~t~~agacat~~g~~tacttatcatata 608  
||||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 1061 gacaacttgaatgttgc~~tt~~c~~t~~agacat~~g~~tacttatcatata 1104

Score = 61.9 bits (31), Expect = 1e-06  
Identities = 73/87 (83%)  
Strand = Plus / Plus

Query: 75 gagtttactaatattgtatcaagcaaaaagctgggtaatgctcagtataaaaaagtatgga 134  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 574 gagtttactaatgttggggaaagccaaaaatggggaaatgctcaatataaaaaatatggc 633

[>] >gi|1212874|emb|X87215.1|CLC3GENE c. limosum C3 gene  
Length = 1022

Score = 99.6 bits (50), Expect = 6e-18  
Identities = 127/153 (83%)  
Strand = Plus / Plus

Query: 498 attacanaatttaaagttagcaaaaggctcaaaggcaggatattgaccctattagtgc 557  
|| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 733 ataacaaaatttaaggttagacggttcaaagcaggatattgaacctattgtacc 792

Query: 558 ttccaggacaacttgaatgttgcttcaga 590  
||| | ||| ||||| ||| ||| ||| ||| |||  
Sbjct: 793 tttaaaggtcaacttgaagtgttgcttcaga 825

Score = 75.8 bits (38), Expect = 9e-11  
Identities = 134/166 (80%)  
Strand = Plus / Plus

Query: 224 caatggatttccttcaaatttaataaaaacaagttgaactttagataatctttataa 283  
||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 459 caatggattacctgcagatataagaaaagaagttgaacaaatagataatcttcactaa 518

Query: 284 aatgaagaccctgaaaatattatgttatttagaggcgacgaccctgcttatttaggaac 343  
||| | ||| ||||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 519 aatgcaaactcctgaaaatattattcttttagaggagatgtcctggatatttaggacc 578

Query: 344 agaatttcaaaacactcttcttaattcaaatggtacaattaataaa 389  
||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 579 ggattttgaaaatactattcttaatagagatggaacaattaataaa 624

[>]gi|33149672|gb|AY330212.1| Cloning vector pT3, complete sequence  
Length = 2551

Score = 67.9 bits (34), Expect = 2e-08  
Identities = 41/42 (97%), Gaps = 1/42 (2%)  
Strand = Plus / Minus

Query: 1 ggatcctctagagtcgacctgcaggcatgcaatgcttattcc 42  
|||||||||||||||||||||||||||||||  
Sbjct: 227 ggatcctctagagtcgacctgcaggcatgcaa-gcttattcc 187

[>]gi|595779|gb|U13871.1|XXU13871 pT7T3D cloning vector, complete sequence  
Length = 2907

Score = 67.9 bits (34), Expect = 2e-08  
Identities = 41/42 (97%), Gaps = 1/42 (2%)  
Strand = Plus / Minus

Query: 1 ggatcctctagagtcgacctgcaggcatgcaatgcttattcc 42  
|||||||||||||||||||||||||||  
Sbjct: 230 ggatcctctagagtcgacctgcaggcatgcaa-gcttattcc 190

[>] >gi|595774|gb|U13869.1|XXU13869 pT7T318U cloning vector, complete sequence  
Length = 2883

Score = 67.9 bits (34), Expect = 2e-08  
Identities = 41/42 (97%), Gaps = 1/42 (2%)  
Strand = Plus / Minus

Query: 1 ggatcctctagagtcgacacctgcaggcatgcaatgcttattcc 42  
|||||||||||||||||||||||||||||||||||||  
Sbjct: 230 ggatcctctagagtcgacacctgcaggcatgcaa-gcttattcc 190

[>] >gi|1149706|emb|X86491.1|CPSPOOA C.perfringens spoOA gene  
Length = 350

Score = 65.9 bits (33), Expect = 9e-08  
Identities = 36/37 (97%)  
Strand = Plus / Plus

Query: 1 ggatcctctagagtcgacacctgcaggcatgctt 37  
|||||||||||||||||||||||||||||  
Sbjct: 275 ggatcctctagagtcgacacctgcaggcatgcaaggctt 311

[>] >gi|31335236|gb|AY292466.1| BAC cloning vector pBACVM4, complete sequence  
Length = 9077

Score = 63.9 bits (32), Expect = 3e-07  
Identities = 32/32 (100%)  
Strand = Plus / Plus

Query: 1 ggatcctctagagtcgacacctgcaggcatgcaa 32  
|||||||||||||||||||||||||  
Sbjct: 1813 ggatcctctagagtcgacacctgcaggcatgcaa 1844

[>] >gi|30424554|gb|AY182782.1| Shuttle vector pSK5640, complete sequence  
Length = 6152

Score = 63.9 bits (32), Expect = 3e-07  
Identities = 32/32 (100%)  
Strand = Plus / Minus

Query: 1 ggatcctctagagtcgacacctgcaggcatgcaa 32  
|||||||||||||||||||||  
Sbjct: 36 ggatcctctagagtcgacacctgcaggcatgcaa 5